## REMARKS

The Specification

The Examiner states that applicants have not complied with one or more conditions for receiving the benefit of an earlier filing date under 35 U.S.C. § 120. The Examiner states that the first page of the specification or the application data sheet must contain a specific reference to the prior application(s).

Applicants draw the Examiner's attention to the application data sheet as filed, which recites the proper priority claim. However, applicants have amended the specification to insert a cross-reference to prior applications as suggested by the Examiner.

The Claims

Applicants have amended claim 48 to recite an isolated DNA molecule and to improve its form. Applicants also have amended claim 48 to recite that the antisense-RNA "is capable of inhibiting the expression of nucleic acid molecules encoding said protein when expressed in a plant cell." Support for this amendment may be found, for example, on page 9, lines 18-24.

Applicants have amended claims 48, 61 and 81 to recite that the protein which is present in plant cells in starch granule-bound form as well as in soluble form "is involved in the phosphorylation of starch when expressed in plants and/or that increases the phosphorylation of glycogen when expressed in *E. coli*." Applicants also have amended claims 48, 61 and 81 to recite stringent hybridization and that the fragment encodes a polypeptide that has the biological activity of the protein of the instant invention. Support

for these amendments may be found throughout the specification. See, e.g., page 4, lines 1-3 and 17-21; page 5, lines 21-26; page 8, lines 8-16 and page 46, lines 16-18.

Applicants have amended claims 51, 53, 54, 60, 65 and 68 to delete reference to cancelled claims. Applicants have amended claims 51, 53 and 54 to insert reference to added claim 99. Applicants have further amended claim 60 to improve its form.

Applicants have amended claims 73, 92 and 93 to recite that the propagation material comprises the plant cell. Support for this amendment may be found, for example, on page 28, lines 20-23.

Applicants have added claims 96-106. Support for added claims 96-98 may be found, for example, on page 6, lines 25-26 and on page 8, lines 5-6. Support for added claims 99-101 may be found, for example, on page 9, lines 36-40. Support for added claims 102-106 may be found, for example, on page 4, lines 1-3; page 5, lines 21-33; page 8, lines 8-16; and page 9, lines 18-24.

None of these amendments adds new matter. Their entry is requested.

The Rejection Under 35 U.S.C. § 112, Second Paragraph

The Examiner has rejected claims 49, 51-57 and 60 under 35 U.S.C. § 112, second paragraph, as indefinite. The Examiner states that the recitation of "said second nucleic acid molecule" in lines 3-4 of claim 49 lacks antecedent basis.

Applicants have cancelled claim 49 and amended claims 51-57 and 60 so that they no longer depend from claim 49, thus obviating this rejection.

The Rejection Under 35 U.S.C. § 101

The Examiner has rejected claims 48 and 60 under 35 U.S.C. § 101 as being directed to non-statutory subject matter. Specifically, the Examiner contends that the claimed DNA or RNA molecules have the same characteristics and utility as those found naturally in the genome. The Examiner recommends amending claims 48 and 60 to recite an isolated nucleic acid molecule.

Applicants have amended claim 48 as suggested by the Examiner, thus obviating the rejection with respect to this claim. Applicants have amended claim 60 to recite "An RNA molecule obtained by transcription of the nucleic acid molecule according to claim 48." An RNA molecule obtained by transcription of an isolated DNA molecule does not have the same characteristics as an RNA molecule found naturally. Therefore, the RNA molecule recited in amended claim 60 is directed to statutory subject matter under 35 U.S.C. § 101.

The Rejections Under 35 U.S.C. § 112, First Paragraph

The Examiner has rejected claims 48-49, 51-57, 60-63, 65-69, 73-76, 81 and 88-95 under 35 U.S.C. § 112, first paragraph, stating that the specification does not enable a person skilled in the art to make and/or use the invention commensurate in scope with the claims. The Examiner acknowledges that the specification enables claims directed to reducing glucan phosphorylase protein levels in a plant using an antisense construct comprising an entire gene encoding a native potato granule-bound protein comprising SEQ ID NO: 2. However, the Examiner contends that the specification does not reasonably provide enablement for claims drawn to any gene from any source or sequence or any

fragment of any length which encodes either a granule-bound or soluble protein, for any ribozyme-mediated gene inhibition, or for any other type of non-exemplified protein reduction.

Specifically, the Examiner states that the specification does not provide guidance for modifying SEQ ID NO: 1; for identifying or isolating a corresponding protein from another plant source; for identifying or isolating any fragment or derivative of SEQ ID NO: 1 which would encode a functional protein involved in starch metabolism; for identifying or isolating any soluble protein; for identifying or isolating any nucleic acid hybridizing to SEQ ID NO: 1 or to a gene encoding SEQ ID NO: 2 which could occur under unspecified hybridization conditions and could encompass a multitude of non-exemplified sequences having a multitude of functions; or for modification of a multitude of uncharacterized sequences which hybridize to an exemplified gene. The Examiner further states that the specification does not provide guidance for ribozyme-mediated gene inhibition as recited in claims 49, 63 and claims depending therefrom or for other types of non-exemplified protein expression reduction methods as recited in claim 61 and claims depending therefrom. The Examiner states that the specification does not provide guidance for evaluating the ability of non-exemplified fragments or genes from non-exemplified sources in antisense orientation for their ability to alter phosphylase protein production or starch accumulation in transformed plants as broadly claimed. Applicants traverse.

As a preliminary matter, applicants note that the protein of the invention (R1 protein) is not a glucan phosphorylase, as stated by the Examiner, but an α-glucan water

dikinase. See, e.g., Ritte et al., "The starch-related R1 protein is an α-glucan water dikinase," Proc. Natl. Acad. Sci. USA 99:7166-71 (2002) (copy enclosed).

As discussed above, applicants have cancelled claims 49 and 63 and amended claims 48, 61 and 81 to recite that the nucleic acid molecules and fragments encode a protein or a polypeptide "that is present in plant cells in starch granule-bound form as well as in soluble form and that is involved in the phosphorylation of starch when expressed in plants and/or that increases the phosphorylation of glycogen when expressed in *E. coli*." Applicants have further amended claims 48, 61 and 81 to recite hybridization "under stringent conditions."

Contrary to the Examiner's assertion, the specification clearly teaches how to identify the fragments and allelic variants recited in the instant claims as well as how to make and use them. See, e.g., page 4, line 13 to page 5, line 13; Examples 6-8; and page 50, line 11 to page 52, line 14. Furthermore, the specification provides guidance for evaluating the ability of the nucleic acid molecules recited in the claims in antisense orientation to alter the amount of protein and thereby starch properties in transformed plants. For example, the specification teaches that reducing the amount of a protein encoded by a nucleic acid molecule in a plant cell as recited in the claims will produce modified starch. See, e.g., page 9, line 18 to page 11, line 8; page 11, line 36 to page 12, line 8; and Example 8, page 43, line 30 to page 48, line 27. The specification further teaches methods for determining whether a plant produces a modified starch. See, e.g., page 33, line 15 to page 34, line 10 and Example 8, page 43, line 30 to page 48, line 27.

The Examiner states that isolation of genes involved in starch accumulation in plants is particularly unpredictable. The Examiner states that Kossmann et al., "Carbohydrate Bioengineering," Progress in Biotechnol., 10: 271-278 (1995) ("Kossmann") teaches the difficulty inherent in isolating individual starch synthesis enzymes and their corresponding genes. The Examiner is mistaken. Kossmann merely states that, in some cases, it is not possible to isolate sufficient soluble starch synthase protein to perform protein sequencing or to raise antibodies. Kossmann never suggests that isolating a hybridizing or homologous nucleic acid molecule to a nucleic acid that is known to encode a protein involved in starch synthesis is difficult. In fact, Kossmann reports the isolation by nucleic acid hybridization of a potato soluble starch synthase cDNA (SSS) using a rice SSS cDNA as a hybridization probe. See, e.g., page 276, first three full paragraphs. Thus, Kossmann teaches that a nucleic acid that encodes a protein with a similar biological activity can be isolated by hybridization. In the present invention, the specification provides nucleic acid sequences that can do just that.

The Examiner also cites Kossmann; Sonnewald et al., "A Second L-Type Isozyme of Potato Glucan Phosphorylase: Cloning, Antisense Inhibition and Expression Analysis," Plant Molec. Biol., 27: 567-576 (1995) ("Sonnewald"); and St.-Pierre et al., "The Starch Phosphorylase Gene Is Subjected to Different Modes of Regulation in Starch-containing Tissues of Potato," Plant Molec. Biol., 30: 1087-1098 (1996) ("St.-Pierre") to support the contention that the process of modifying starch accumulation in transgenic plants is "particularly unpredictable." The Examiner states that undue experimentation would be required to demonstrate that reducing the amount of a protein encoded by a

nucleic acid molecule recited in the claims would confer phenotypic changes to plants transformed with antisense constructs. Applicants traverse.

The Examiner cites particular studies in Kossmann, Sonnewald and St.-Pierre that do not relate to the transgenic plants described in the instant application. Specifically, the Examiner states that Kossmann teaches the lack of influence of antisense potato starch accumulation genes on branching or phosphate content of starch (p. 5, Office Action). The Examiner cites reports in Kossmann wherein the expression of an antisense RNA specific for a GBSS II protein or potato branching enzyme in transgenic potato plants did not result in any changes in the amylose content of the starch produced. The Examiner cites a report in Sonnewald that states that antisense RNA repression of the leaf L-type starch phosphorylase gene had no significant influence on starch accumulation in leaves of transgenic potato plants. The Examiner cites reports in St.-Pierre that suggest that potato starch phosphorylase gene expression may involve factors other than rates of transcription.

In contrast to Kossmann, the present application teaches and exemplifies transgenic plants that express antisense RNA to the nucleic acid molecules recited in the claims synthesize a starch with a reduced phosphate content. See, e.g., page 13, line 39 to page 14, line 2, and Example 8 (pages 43-48). Furthermore, the specification teaches and exemplifies microorganisms expressing one of the nucleic acid molecules recited in the claims synthesize glycogen with increased phosphate content. See, e.g., Example 9, pages 49-52. In addition, the specification teaches that modified starch can be produced by reducing the levels of a protein encoded by the nucleic acid molecule recited in the claims by a cosuppression effect. See page 9, lines 18-24. Thus one of skill in the art would

expect that a transgenic plant according to this invention would produce a modified starch. Further, unlike Sonnewald, the present invention shows a correlation between reducing the levels of a protein encoded by the nucleic acid molecule recited in the claims and formation of modified starch. Still further, the Examiner has provided no reasons why the 5' region of a potato L-type starch phosphorylase gene of St.-Pierre would be predictive of the effect of reducing the levels of a protein encoded by the nucleic acid molecule as recited in the instant claims.

The Examiner cites Evans et al., "The Effects of Ribozymes on Gene Expression in Plants," Biochem. Soc. Trans., 20: 344S (1992); Mazzolini et al., "Assaying Synthetic Ribozymes in Plants: High-level Expression of a Functional Hammerhead Structure Fails to Inhibit Target Gene Activity in Transiently Transformed Protoplasts," Plant Molec. Biol., 20: 715-731 (1992) ("Mazzolini"); and Kull et al., "Genetic Engineering of Potato Starch Composition: Inhibition of Amylose Biosynthesis in Tubers from Transgenic Potato Lines by the Expression of Antisense Sequences of the Gene for Granule-bound Starch Synthase," J. Genet. & Breed., 49: 69-76 (1995) ("Kull") to support the contention that the use of ribozymes to inhibit genes or change phenotypes has not been demonstrated to be effective in plants. According to the Examiner, undue experimentation would be required to evaluate and obtain successful gene inhibition with ribozymes.

Applicants' cancellation of claims 49 and 63 obviates the rejection with respect to ribozymes. Applicants expressly reserve the right to pursue the canceled subject matter in subsequent application(s) claiming priority herefrom.

The Examiner also states that Newman et al., "Genes Galore: a Summary of Methods for Accesssing Results from Large-scale Partial Sequence of Anonymous Arabidopsis cDNA Clones," Plant Physiol. 106:1241-55 (1994) ("Newman") teaches that fragments of the exemplified genes are found in an Arabidopsis gene of unidentified function. The Examiner contends that tranformation of a plant with fragments of the gene in Newman is unlikely to affect starch accumulation. The Examiner provides no discussion as to why Newman, which recites a list of expressed sequence tags (ESTs) and provides no functional data or transgenic plant data, relates to the predictability regarding whether reducing the amount of a protein encoded by the nucleic acid molecules as recited in the instant claims would produce a modified starch in a plant. As discussed above, transgenic plants comprising the claimed nucleic acid molecules are fully enabled by the specification.

Finally, the Examiner states that In re Bell, 26 USPQ2d 1529, 1532 (Fed. Cir. 1993) ("Bell") and In re Deuel, 34 USPQ2d 1210 (Fed. Cir. 1995) ("Deuel") teach that the mere existence of a protein does not enable claims drawn to a nucleic acid encoding that protein. The Examiner is mistaken.

Enablement was not the issue in Bell or Deuel. In Deuel, the court states that "we will not address whether claims 4 and 6 satisfy the enablement requirement of § 112, first paragraph." Further, unlike Bell and Deuel, the present application provides a structural and functional description for the nucleic acid molecules recited in the claims. Thus, Bell and Deuel are inapposite to the instant case, legally and factually.

The Examiner also has rejected claims 48-49, 51-57, 60-63, 65-69, 73-76, 81 and 88-95 under 35 U.S.C. § 112, first paragraph, as lacking adequate written description.

The Examiner states that the claims are broadly drawn to a multitute of non-exemplified sequences and fragments from multiple sources. The Examiner contends that the specification lacks guidance for obtaining or characterizing any fragments or derivatives or for obtaining or characterizing any ribozyme-encoding sequence. The Examiner contends that one skilled in the art would not recognize that applicants were in possession of the invention as claimed. Applicants traverse.

As discussed above, the specification clearly teaches how to identify the fragments and allelic variants recited in the instant claims as well as how to make and use them. See, e.g., page 5, lines 3-13; Examples 6-8; and page 50, line 11 to page 52, line 14. Furthermore, the specification provides guidance for evaluating the ability of the nucleic acid molecules recited in the claims in antisense orientation to alter the amount of protein and thereby starch properties in transformed plants. For example, the specification teaches that reducing the amount of a protein encoded by a nucleic acid molecule in a plant cell as recited in the claims will produce modified starch. See, e.g., page 9, line 18 to page 11, line 8; page 11, line 36 to page 12, line 8;and Example 8, page 43, line 30 to page 48, line 27. The specification further teaches methods for determining whether a plant produces a modified starch. See, e.g., page 33, line 15 to page 34, line 10 and Example 8, page 43, line 30 to page 48, line 27. Thus, contrary to the Examiner's assertion, one skilled in the art would clearly recognize that applicants were in possession of the invention as claimed.

The Examiner states that Amgen Inc. v. Chugai Pharmaceutical Co., Ltd., 18 USPQ2d 1016, 1021, 1027 (Fed. Cir. 1991) ("Amgen") teaches that a gene is not reduced to practice until the inventor can define it by its physical or chemical properties, and that

disclosure of a few gene sequences did not enable claims broadly drawn to any analog thereof. The Examiner also states that University of California v. Eli Lilly and Co., 43 USPQ2d 1893 (Fed. Cir. 1997) ("Lilly") teaches that the disclosure of a process for obtaining cDNA from a particular organism and a description of the encoded protein fails to provide an adequate written description of the actual cDNA from that organism, despite the disclosure of a cDNA encoding that protein from another organism. The Examiner's citation of Amgen and Lilly is inapposite.

Unlike Amgen, the nucleic acid molecules recited in the instant claims are structurally and functionally defined. The DNA molecules of the invention are described structurally and functionally as encoding an antisense-RNA which is capable of inhibiting, when expressed in a plant cell, expression of a protein encoded by a structurally and functionally defined nucleic acid molecule. The nucleic acids molecules are described structurally because they must hybridize under stringent conditions to a nucleic acid molecule having the nucleotide sequence of SEQ ID NO: 1 or encoding the amino acid sequence of SEQ ID NO: 2. The nucleic acid molecules are also described functionally, in that they are able to reduce the gene expression of a gene encoding a protein that is present in plant cells in starch granule-bound form as well as in soluble form and that is involved in the phosphorylation of starch when expressed in plants and/or that increases the phosphorylation of glycogen when expressed in *E. coli*. Still further, the specification discloses a relationship between the structure of the nucleic acid molecule and the function of the polypeptide it encodes. See, e.g., page 5, lines 37-39. Thus, the specification describes the DNA molecules and the nucleic acid molecules recited in the claims by their physical properties.

The Rejections under 35 U.S.C. § 102(b)

The Examiner has rejected claims 48, 51-54, 60-62, 68, 69, 73-76, 81 and 88-95 under 35 U.S.C. § 102(b) as anticipated by Kull. The Examiner states that Kull teaches a nucleic acid molecule comprising fragments of at least one nucleotide of SEQ ID NO: 1. The Examiner contends that these fragments constitute derivatives of SEQ ID NO: 1 or would hybridize to SEQ ID NO: 1 under conditions of at least low stringency. The Examiner further states that the nucleic acid molecule described in Kull was inserted into a vector in antisense orientation and introduced into potato plants. Finally, the Examiner contends that cold-sweetening would have been an inherent property. Applicants traverse.

As discussed above, applicants have amended claims 48, 61 and 81 to recite that the fragment has specific properties and that hybridization is performed under stringent conditions. Kull describes a potato *Waxy* gene encoding a protein, granule-bound starch synthase (GBSS), an enzyme which catalyzes the transfer of a glucosyl residue of ADP-glucose to α-1,4-glucans. GBSS is not involved in phosphorylation of starch when expressed in plants and which does not increase the phosphorylation of glycogen when expressed in *E. coli*. Further, contrary to the Examiner's contention, inhibition of the granule-bound starch synthase I gene (GBSS-I) would not be expected to have the same effects as inhibition of R1 protein with respect to reduction of cold-sweetening. Thus, Kull does not teach or describe the nucleic acid molecules of the invention. Accordingly, Kull does not anticipate the isolated nucleic acid molecules of the invention and therefore does not anticipate a cell comprising the isolated nucleic acid molecules of the invention, a plant comprising such a cell or methods of using them.

The Examiner has rejected claims 73 and 92-93 under 35 U.S.C. § 102(b) as allegedly anticipated by or, in the alternative, under 35 U.S.C. § 103(a) as obvious over St.-Pierre. The Examiner states that the claims fail to recite that the transgene is retained in the claimed propagation material. The Examiner contends that the claims read on propagation material of wild-type potato.

As discussed above, applicants have amended claims 73 and 92-93 to recite that the propagation material comprises the transgenic plant cell, thus obviating this rejection.

The Rejection under 35 U.S.C. § 103(a)

The Examiner has rejected claims 48-49, 51-57, 60-63, 65-69, 73-76, 81 and 88-95 under 35 U.S.C. § 103(a) as being unpatentable over Kull taken with Bird et al., United States Patent 6,013,861 ("Bird"). The Examiner states that Kull teaches potato plants transformed with antisense constructs to fragments or derivatives of a glucan phosphorylase gene but does not teach the use of another antisense construct corresponding to another starch metabolism gene. The Examiner states that Bird suggests the inhibition of multiple starch synthesis enzymes for the production of starch with particular properties and suggest potato transformation. The Examiner contends that it would have been obvious to one of ordinary skill in the art to use the method taught by Kull modified by incorporating additional antisense constructs to known starch synthesis genes as suggested by Bird. Applicants traverse.

As discussed above, applicants have amended claims 48, 61 and 81 to recite that the fragment "encodes a protein that is present in plant cells in starch granule-bound

form as well as in soluble form and that is involved in the phosphorylation of starch when expressed in plants and/or that increases the phosphorylation of glycogen when expressed in *E. coli*." Further, as discussed above, Kull does not teach or suggest the claimed nucleic acid molecules of the invention. Bird suggest the inhibition of genes encoding soluble starch synthase and branching enzymes but not R1 protein. Bird, like Kull does not disclose nucleic acid molecules encoding R1 protein. Thus, Bird, does not rectify the deficiency in Kull and these references, either alone or taken together, do not render the amended claims obvious.

Conclusion

For the reasons presented above, applicants request that the Examiner allow claims 48, 51-57, 60-62, 65-69, 73-76, 81 and 88-106 to issue.

Respectfully submitted,

Karen E. Brown

James F. Haley, Jr.(Reg. No. 27,794)
Attorney for Applicants
Karen E. Brown (Reg. No. 43,866)
Grant Kalinowski (Reg. No. 48,314)
Agents for Applicants

FISH & NEAVE
Customer No. 1473
1251 Avenue of the Americas
New York, New York 10020-1104
Tel.: (212) 596-9000
Fax: (212) 596-9090

Copy of claims 48, 51, 53, 54, 60, 61, 65, 68, 73, 81, 92 and 93
marked up pursuant to 37 C.F.R. § 1.121(c)(1)(ii) to show changes made

48. (Twice Amended) [A] An isolated DNA molecule encoding an antisense-RNA complementary to a transcript of a nucleic acid molecule encoding a protein which is present in plant cells in starch granule-bound form as well as in soluble form and that is involved in the phosphorylation of starch when expressed in plants and/or that increases the phosphorylation of glycogen when expressed in *E. coli*, said nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule [encoding] comprising a nucleotide sequence that encodes a protein [with] having the [amino-acid] amino acid sequence [indicated in] of SEQ ID NO: 2;

(b) a nucleic acid molecule comprising the coding region of the nucleotide sequence [indicated in] of SEQ ID NO: 1;

(c) a nucleic acid molecule [hybridizing to a] that hybridizes to the nucleic acid molecule of (a) or (b) under stringent conditions;

(d) a nucleic acid molecule the sequence of which is degenerate as a result of the genetic code to a nucleic acid molecule of [(a) or (b)] (a), (b) or (c); and

(e) a fragment[, derivative] or allelic variant of a nucleic acid molecule of (a), (b), (c), or (d), wherein the fragment or allelic variant encodes a polypeptide that is present in plant cells in starch granule-bound form as well as in soluble form and that is

involved in the phosphorylation of starch when expressed in plants and/or that increases the phosphorylation of glycogen when expressed in *E. coli*,

wherein said antisense-RNA is capable of inhibiting the expression of nucleic acid molecules encoding said protein when expressed in a plant cell.

51. (Twice Amended) A vector comprising the DNA molecule according to claim 48 or [49] 99.

53. (Twice Amended) A host cell comprising the DNA molecule according to claim 48 or [49] 99 or comprising a vector comprising said DNA molecule.

54. (Twice Amended) A transgenic plant cell comprising the DNA molecule according to claim 48 or [49] 99, wherein said DNA molecule is operably linked to regulatory elements ensuring transcription in a plant cell.

60. (Twice Amended) An RNA molecule [obtainable] obtained by transcription of the [nucleic acid] DNA molecule according to claim 48 or [49] 99.

61. (Twice Amended) A method for producing a transgenic plant cell synthesizing a modified starch comprising the step of reducing in the cell the amount of a protein which is present in the plant cell in starch granule-bound form as well as in soluble form and that is involved in the phosphorylation of starch when expressed in plants and/or that increases the phosphorylation of glycogen when expressed in *E. coli*, said protein encoded by a nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule encoding a protein with the amino-acid sequence indicated in SEQ ID NO: 2;

(b) a nucleic acid molecule comprising the coding region of the nucleotide sequence indicated in SEQ ID NO: 1;

(c) a nucleic acid molecule hybridizing to a nucleic acid molecule of (a) or (b) under stringent conditions;

(d) a nucleic acid molecule the sequence of which is degenerate as a result of the genetic code to a nucleic acid molecule of (a) or (b); and

(e) a fragment, derivative or allelic variant of a nucleic acid molecule of (a), (b), (c), or (d), wherein the fragment, derivative or allelic variant encodes a polypeptide that is present in plant cells in starch granule-bound form as well as in soluble form and that is involved in the phosphorylation of starch when expressed in plants and/or that increases the phosphorylation of glycogen when expressed in *E. coli*;

wherein said [reducing] reduction of the amount of said protein results in the plant cell producing a modified starch.

65. (Twice Amended) The method of [any one of claims 61 to 63] claim 61 or 62, wherein the enzyme activity of at least one further enzyme involved in the starch biosynthesis and/or modification is reduced.

68. (Twice Amended) A plant cell obtainable by the method of [any one of claims 61 to 63] claim 61 or 62.

73. (Twice Amended) A propagation material of the plant according to claim 69, wherein the propagation material comprises the plant cell.

81. (Twice Amended) The transgenic plant cell of claim 54 wherein the amount of a protein is reduced in the transgenic plant cell when compared to the wild-type plant cell, wherein the protein is present in the plant cell in starch granule-bound form as well as in soluble form and that is involved in the phosphorylation of starch when expressed in plants and/or that increases the phosphorylation of glycogen when expressed in *E. coli*, and wherein the protein is encoded by a nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule encoding a protein with the amino-acid sequence indicated in SEQ ID NO: 2;

(b) a nucleic acid molecule comprising the coding region of the nucleotide sequence indicated in SEQ ID NO: 1;

(c) a nucleic acid molecule hybridizing to a nucleic acid molecule of (a) or (b) under stringent conditions;

(d) a nucleic acid molecule the sequence of which is degenerate as a result of the genetic code to a nucleic acid molecule of (a) or (b); and

(e) a fragment, derivative or allelic variant of a nucleic acid molecule of (a), (b), (c), or (d), wherein the fragment, derivative or allelic variant encodes a polypeptide that is present in plant cells in starch granule-bound form as well as in soluble form and that

is involved in the phosphorylation of starch when expressed in plants and/or that increases the phosphorylation of glycogen when expressed in *E. coli*.

92. (Amended) A propagation material of the plant according to claim 88, wherein the propagation material comprises the plant cell.

93. (Amended) A propagation material of the plant according to claim 89, wherein the propagation material comprises the plant cell.